52. (New)   The method of claim 51, wherein the at least one *Staphylococcus aureus* sequence region has a mutation rate sufficient to differentiate between subspecies of *Staphylococcus aureus* to determine phylogenetic relatedness and to track the microorganism.

53. (New)   The method of claim 51, wherein the *Staphylococcus aureus* sequence regions comprise a region of variable number tandem repeats.

54. (New)   The method of claim 53, wherein the region of variable number of tandem repeats comprise at least one sequence selected from the group consisting of SEQ ID NO 55, SEQ ID NO 57, SEQ ID NO 58, SEQ ID NO 59, SEQ ID NO 60, SEQ ID NO 61, SEQ ID NO 62, SEQ ID NO 63, SEQ ID NO 64, SEQ ID NO 65, SEQ ID NO66, SEQ ID NO 67, SEQ ID NO 68, SEQ ID NO 69, SEQ ID NO 70, SEQ ID NO 71, SEQ ID NO 72, SEQ ID NO 73, SEQ ID NO 74, SEQ ID NO 78, SEQ ID NO 79, and SEQ ID NO 80.

55. (New)   The method of claim 54, wherein the region of variable number of tandem repeats further comprise at least one point mutation in at least one sequence.

56. (New)   The method of claim 55, wherein the number of point mutations is sufficient to identify the sequence and determine the phylogenetic relatedness of microorganisms including the sequence in their genome.

57. (New)   The method of claim 55, wherein the at least one point mutation is not in the first three nucleotides of the at least one sequence.

58. (New)   The method of claim 51, wherein the forward primer comprises SEQ ID NO 75 and the reverse primer comprises SEQ ID NO 76.

59. (New)   The method of claim 58, wherein the forward primer comprises SEQ ID NO 76 and the reverse primer comprises SEQ ID NO 77.

60. (New)   The method of claim 54, wherein the first three nucleotides of the at least one sequence are GAT or GAC.

61. (New)   The method of claim 54, wherein the region of variable number of tandem repeats comprises more than one copy of at least one sequence selected from the

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group consisting of SEQ ID NO 55, SEQ ID NO 57, SEQ ID NO 58, SEQ ID NO 59, SEQ ID NO 60, SEQ ID NO 61, SEQ ID NO 62, SEQ ID NO 63, SEQ ID NO 64, SEQ ID NO 65, SEQ ID NO66, SEQ ID NO 67, SEQ ID NO 68, SEQ ID NO 69, SEQ ID NO 70, SEQ ID NO 71, SEQ ID NO 72, SEQ ID NO 73, SEQ ID NO 74, SEQ ID NO 78, SEQ ID NO 79, and SEQ ID NO 80.

62. (New)   The method of claim 51, wherein the historical sequence data comprises the sequence of SEQ ID NO 54.

63. (New)   The method of claim 53, wherein the region of variable number of tandem repeats is sufficient to determine the phylogenetic relatedness between the microorganism sample and the plurality of historical samples stored in the database.

64. (New)   A method for identifying a subspecies of *Enterococcus Faecalis*, the method comprising:
    obtaining a sample of a microorganism;
    sequencing a first region of a nucleic acid from the microorganism sample;
    comparing the first sequenced region with historical sequence data stored in a database, the historical sequence data comprising at least one *Enterococcus Faecalis* sequence region; and
    determining a measure of phylogenetic relatedness between the microorganism sample and a plurality of historical samples stored in the database;
    wherein the at least one *Enterococcus Faecalis* sequence region further comprises a forward primer upstream of the sequence and a reverse primer downstream of the sequence, and the forward primer and the reverse primer permit identification of a region of variable number tandem repeats.

65. (New)   The method of claim 64, wherein the at least one *Enterococcus Faecalis* sequence region has a mutation rate sufficient to differentiate between subspecies of *Enterococcus Faecalis* to determine phylogenetic relatedness and to track the microorganism.

66. (New)   The method of claim 64, wherein the *Enterococcus Faecalis* sequence regions comprise a region of variable number tandem repeats.

67. (New)   The method of claim 66, wherein the region of variable number of tandem repeats comprise at least one sequence selected from the group consisting of SEQ ID

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NO 24, SEQ ID NO 25, SEQ ID NO 26, SEQ ID NO 27, SEQ ID NO 28, SEQ ID NO 29, SEQ ID NO 30, SEQ ID NO 31, SEQ ID NO 32, SEQ ID NO 33, SEQ ID NO 34, SEQ ID NO 35, and SEQ ID NO 36.

68. (New)   The method of claim 67, wherein the region of variable number of tandem repeats further comprise at least one point mutation in at least one sequence.

69. (New)   The method of claim 68, wherein the number of point mutations is sufficient to identify the sequence and determine the phylogenetic relatedness of microorganisms including the sequence in their genome.

70. (New)   The method of claim 68, wherein the at least one point mutation is not in the first three nucleotides of the at least one sequence.

71. (New)   The method of claim 64, wherein the forward primer comprises SEQ ID NO 37 and the reverse primer comprises SEQ ID NO 38.

72. (New)   The method of claim 67, wherein the region of variable number of tandem repeats comprises more than one copy of at least one sequence selected from the group consisting of SEQ ID NO 24, SEQ ID NO 25, SEQ ID NO 26, SEQ ID NO 27, SEQ ID NO 28, SEQ ID NO 29, SEQ ID NO 30, SEQ ID NO 31, SEQ ID NO 32, SEQ ID NO 33, SEQ ID NO 34, SEQ ID NO 35, and SEQ ID NO 36.

73. (New)   The method of claim 64, wherein the historical sequence data comprises the sequence of SEQ ID NO 23.

74. (New)   The method of claim 67, wherein the first three nucleotides of the at least one sequence are GTA or GTG.

75. (New)   The method of claim 66, wherein the region of variable number of tandem repeats is sufficient to determine the phylogenetic relatedness between the microorganism sample and the plurality of historical samples stored in the database.

76. (New)   A method for identifying a subspecies of *Helicobacter pylori*, the method comprising:

obtaining a sample of a microorganism;

sequencing a first region of a nucleic acid from the microorganism sample;

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comparing the first sequenced region with historical sequence data stored in a database, the historical sequence data comprising at least one *Helicobacter pylori* sequence region; and

determining a measure of phylogenetic relatedness between the microorganism sample and a plurality of historical samples stored in the database;

wherein the at least one *Helicobacter pylori* sequence region further comprises a forward primer upstream of the sequence and a reverse primer downstream of the sequence, and the forward primer and the reverse primer permit identification of a region of variable number tandem repeats.

77. (New)   The method of claim 76, wherein the at least one *Helicobacter pylori* sequence region has a mutation rate sufficient to differentiate between subspecies of *Helicobacter pylori* to determine phylogenetic relatedness and to track the microorganism.

78. (New)   The method of claim 76, wherein the *Helicobacter pylori* sequence regions comprise a region of variable number tandem repeats.

79 (New)   The method of claim 78, wherein the region of variable number of tandem repeats comprise at least one sequence of SEQ ID NO 50.

80. (New)   The method of claim 79, wherein the region of variable number of tandem repeats further comprise at least one point mutation in at least one sequence.

81. (New)   The method of claim 80, wherein the number of point mutations is sufficient to identify the sequence and determine the phylogenetic relatedness of microorganisms including the sequence in their genome.

82. (New)   The method of claim 80, wherein the at least one point mutation is not in the first three nucleotides of the at least one sequence.

83. (New)   The method of claim 76, wherein the forward primer comprises SEQ ID NO 51 and the reverse primer comprises SEQ ID NO 52.

84. (New)   The method of claim 79, wherein the region of variable number of tandem repeats comprises more than one copy of at least one sequence of SEQ ID NO 50.

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